JAFROC 4.0 User Manual

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Windows XP, Vista and Windows 7 integrated software to perform JAFROC analysis and sample size estimation for FROC and ROC studies

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Features

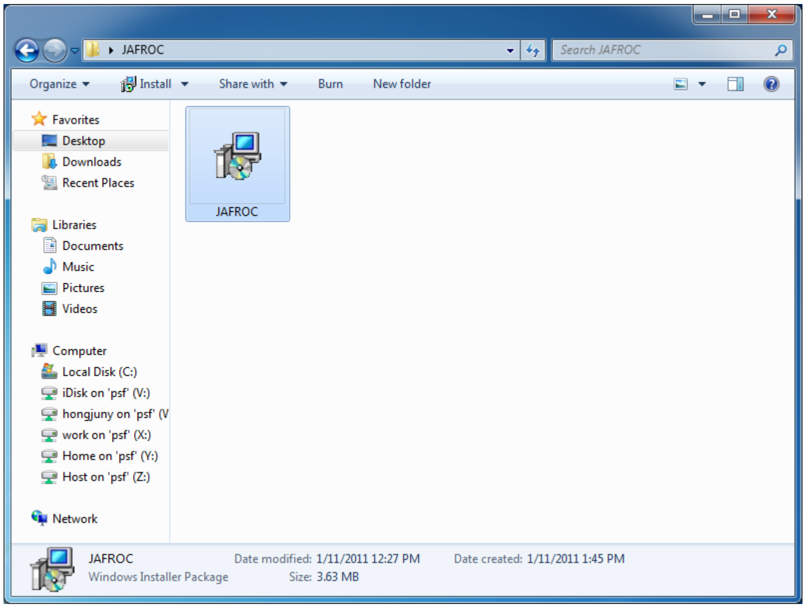
JAFROC analysis is described in Ref. (1). Basic ROC references are (2-4).

1. Standalone windows compatible software (XP, Vista, 7).
2. Convenient FROC raw data plotting: this is a quick way to check the quality of the FROC data and train readers in optimal usage of the ratings scale (5).
3. Integrated plotting routine – uses maximum likelihood method to fit the search model (6, 7) to ROC, FROC and AFROC data.
4. Integrated sample size analysis using an adaptation of the Hillis-Berbaum method (8).
5. Ability to perform user-defined FROC analysis by accessing the built in DLLs. See JAFROC Development Kit Guide.doc for further details.

Installing the software

Install "Microsoft Visual C++ 2010 Redistributable Package (x86)" before installing JAFROC software. It is available at http://www.microsoft.com/downloads/en/details.aspx?familyid=A7B7A05E-6DE6-4D3A-A423-37BF0912DB84&displaylang=en. Search for "Microsoft Visual C++ 2010 Redistributable Package (x86)" on Google to get to this site.

Double-click JAFROC.MSI file.



JAFROC
Windows Installer Package
Date modified: 1/11/2011 12:27 PM
Size: 3.63 MB
Date created: 1/11/2011 1:45 PM

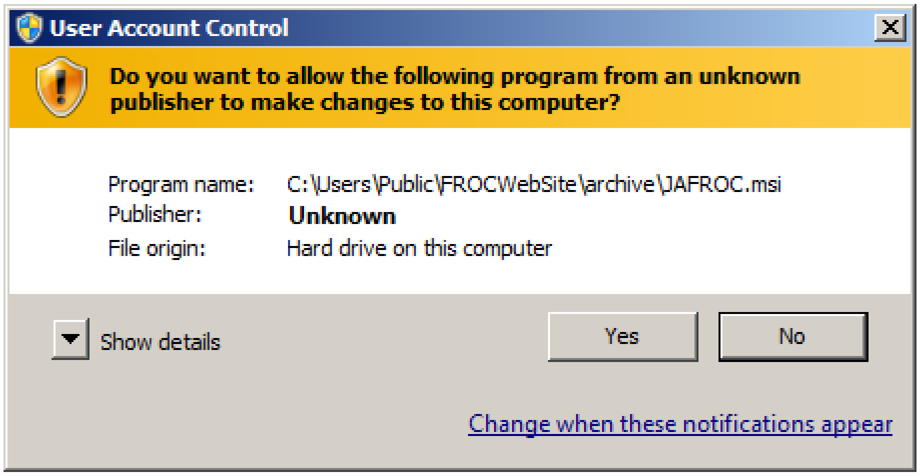
Installation creates a “JAFROC” folder in the “Program Files” folder and “JAFROC Data” folder in “Documents” folder and copies a sample JAFROC data file "DataFile.xls" and “plot_template.xls” file to this folder. Click on "Next"

Welcome to the JAFROC Setup Wizard

The installer will guide you through the steps required to install JAFROC on your computer.

WARNING: This computer program is protected by copyright law and international treaties. Unauthorized duplication or distribution of this program, or any portion of it, may result in severe civil or criminal penalties, and will be prosecuted to the maximum extent possible under the law.

If running under Windows 7 the following screen may appear:

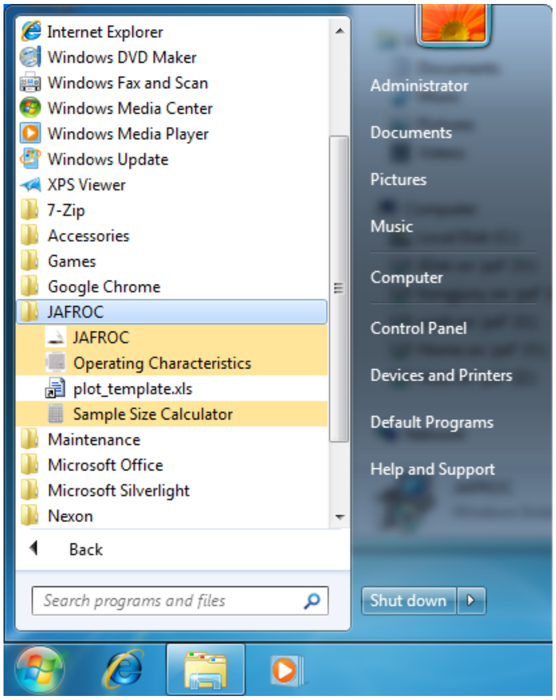


Do you want to allow the following program from an unknown publisher to make changes to this computer?

Program name: C:\Users\Public\FROCWebSite\archive\JAFROC.msi
Publisher: **Unknown**
File origin: Hard drive on this computer

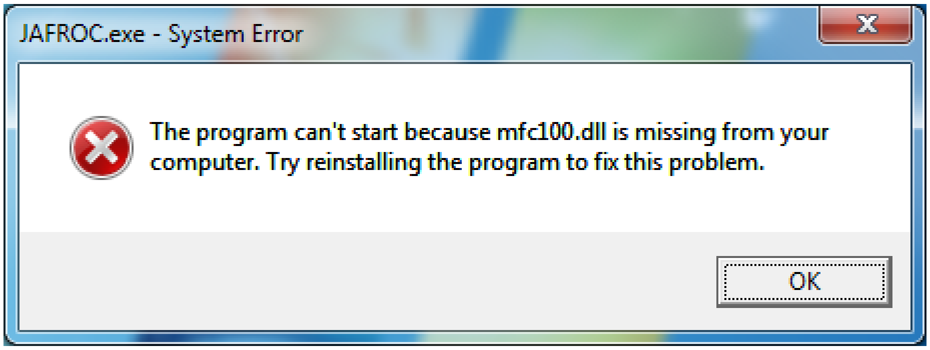
Click on "Yes".

After installation, click on [Start] menu and check that the JAFROC folder was created with four icons in.



If you get the error message shown below when you start JAFROC software, try installing "Microsoft Visual C++ 2010 Redistributable Package (x86)" available at http://www.microsoft.com/downloads/en/details.aspx?familyid=A7B7A05E-6DE6-4D3A-A423-37BF0912DB84&displaylang=en

and restart JAFROC.

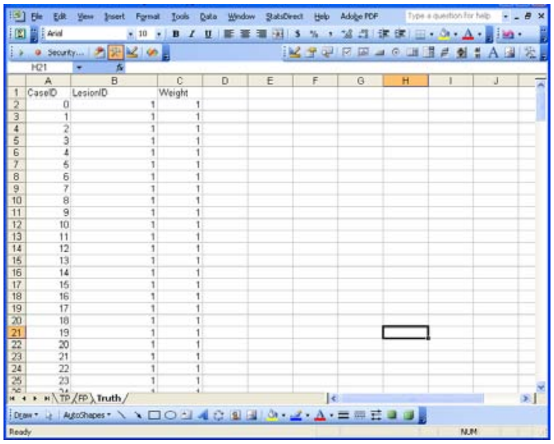

JAFROC.exe - System Error

The program can't start because mfc100.dll is missing from your computer. Try reinstalling the program to fix this problem.

Data format

For a quick understanding of the format see the sample input file "Data3.xls" included in the zip file. The file plot_template.xls is not an input file. It is intended for creating FROC and AFROC plots. Note: text input format is no longer supported.

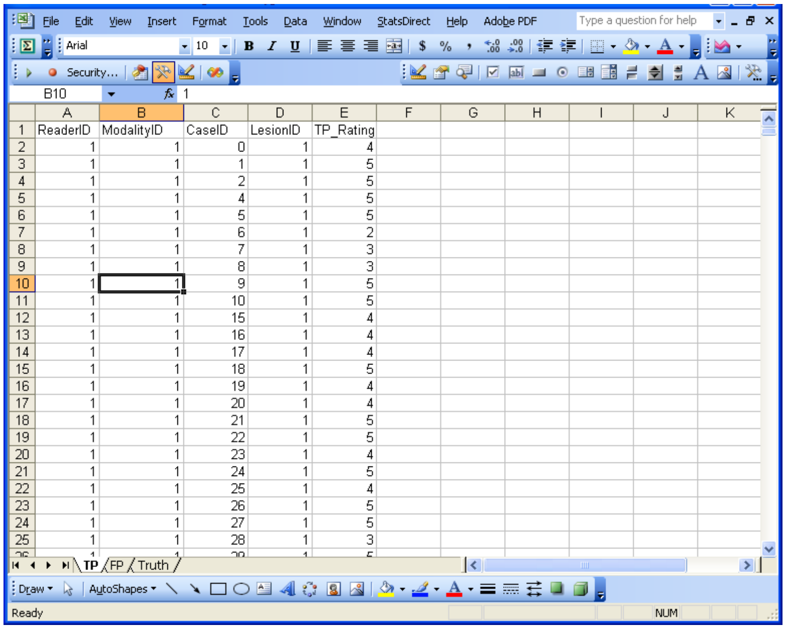
Truth worksheet



	A	B	C
1	CaseID	LesionID	Weight
2	0	1	1
3	1	1	1
4	2	1	1
5	3	1	1
6	4	1	1
7	5	1	1
8	6	1	1
9	7	1	1
10	8	1	1
11	9	1	1
12	10	1	1
13	11	1	1
14	12	1	1
15	13	1	1
16	14	1	1
17	15	1	1
18	16	1	1
19	17	1	1
20	18	1	1
21	19	1	1
22	20	1	1
23	21	1	1
24	22	1	1
25	23	1	1

Label	**Meaning**
CaseID	This **integer** field identifies the case (or patient or image). Cases must be **uniquely** labeled with integers; the integers do not have to be sequentially numbered.
LesionID	This **integer** field tells the program how many lesions are in a particular image and uniquely identifies them. If this number is zero the case is considered to be normal. If a case has multiple lesions then these must be uniquely identified with integers (they do not need to be sequential). For weighted analysis the lesion IDs in the Truth and TP worksheets must refer to the same lesions. For un-weighted analysis matching is not necessary. E.g., 11, 2, 31 and 4 for an abnormal case with 4-lesions; 1 and 2 for an abnormal case with 2-lesions; 0 for a normal case.
Weight	This **positive** **floating-point** value is the weight corresponding to the lesion ID. For each abnormal case there must be as many weights as there are lesions. e.g., 0.1, 0.2, 0.3, and 0.4 for a 4-lesion case; 0.5 and 0.5 for a 2-lesion case (equally weighted). Note that the sum of weights for a case must be 1.0 (to within 1%). For a normal case the weight field must be zero.

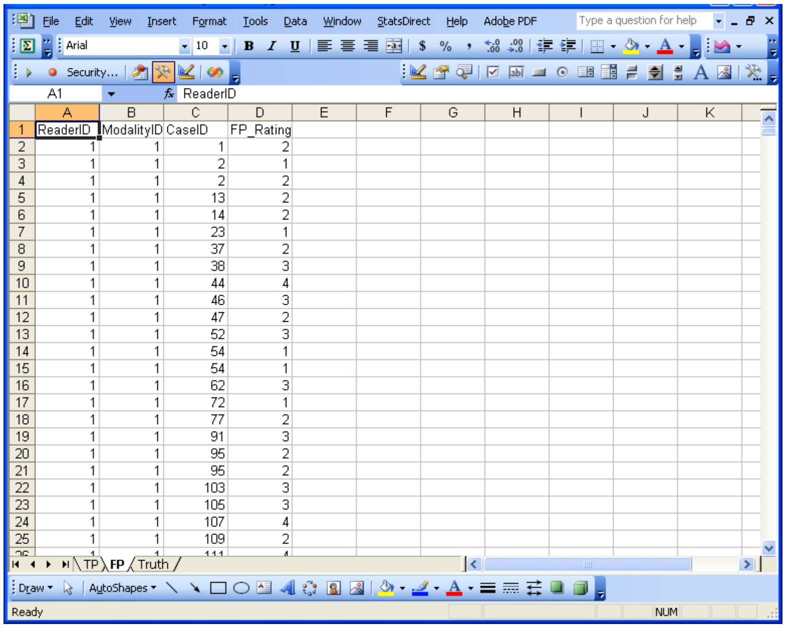
TP (lesion localization) Worksheet



ReaderID	ModalityID	CaseID	LesionID	TP_Rating
1	1	0	1	4
1	1	1	1	5
1	1	2	1	5
1	1	4	1	5
1	1	5	1	5
1	1	6	1	2
1	1	7	1	3
1	1	8	1	3
1	1	9	1	5
1	1	10	1	5
1	1	15	1	4
1	1	16	1	4
1	1	17	1	4
1	1	18	1	5
1	1	19	1	4
1	1	20	1	4
1	1	21	1	5
1	1	22	1	5
1	1	23	1	4
1	1	24	1	5
1	1	25	1	4
1	1	26	1	5
1	1	27	1	5
1	1	28	1	3

Label	**Meaning**
ReaderID	This **integer** field identifies the readers. The entries must be unique integers, e.g., 1 or 2 or 3 for 3 readers.
ModalityID	This **integer** field identifies the modalities, e.g., 1 or 2 for 2 modalities.
CaseID	As in Table 1
LesionID	As in Table 1
TP_Rating	This **positive integer / floating-point** value is the rating assigned to a particular TP mark. **Higher numbers represent greater confidence** that the location is actually a lesion. For images with multiple lesions the ratings must correspond to the LesionIDs in the truth table unless the lesions are equally weighted. Otherwise the rating associated with a particular lesion will not match its weight.

FP (non-lesion localization) Worksheet

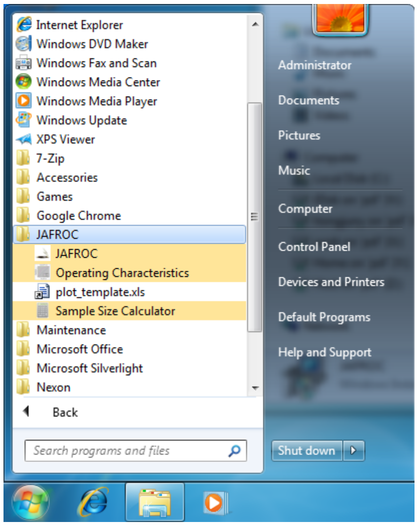


	A	B	C	D
1	ReaderID	ModalityID	CaseID	FP_Rating
2	1	1	1	2
3	1	1	2	1
4	1	1	2	2
5	1	1	13	2
6	1	1	14	2
7	1	1	23	1
8	1	1	37	2
9	1	1	38	3
10	1	1	44	4
11	1	1	46	3
12	1	1	47	2
13	1	1	52	3
14	1	1	54	1
15	1	1	54	1
16	1	1	62	3
17	1	1	72	1
18	1	1	77	2
19	1	1	91	3
20	1	1	95	2
21	1	1	95	2
22	1	1	103	3
23	1	1	105	3
24	1	1	107	4
25	1	1	109	2

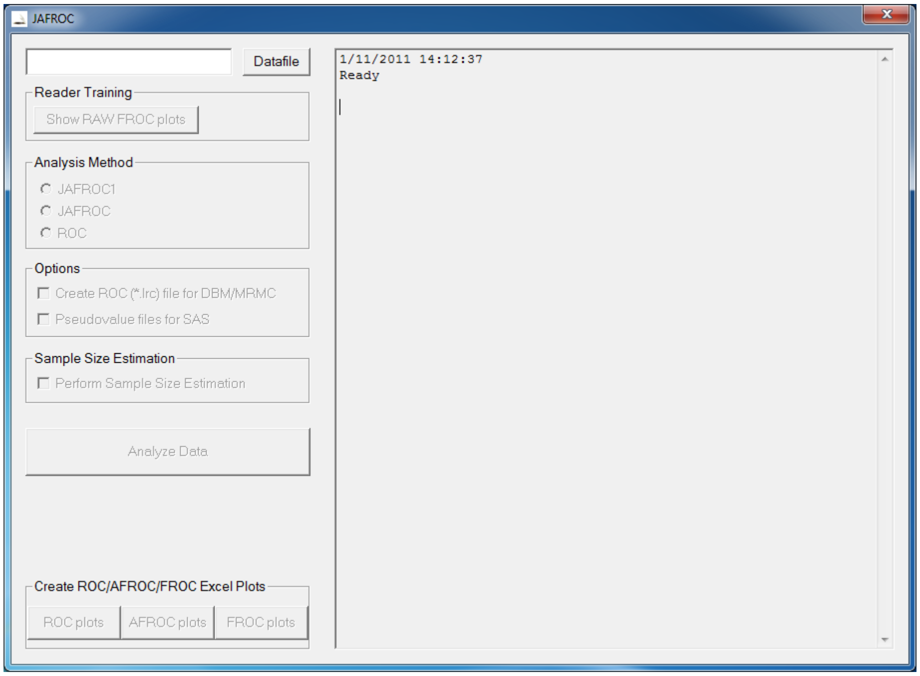
Label	**Meaning**
ReaderID	As in Table 2
ModalityID	As in Table 2
CaseID	**As in Table 1, but on this sheet the cases must be grouped: if two or more false positives occur for the same reader, modality and case then they should appear consecutively and not be separated by data for other cases.**
FP_Rating	This **positive integer / floating-point** value is the rating assigned to a particular FP mark. Multiple false positive are indicated on multiple lines.

Running the software

Click [Start] menu and select JAFROC icon.

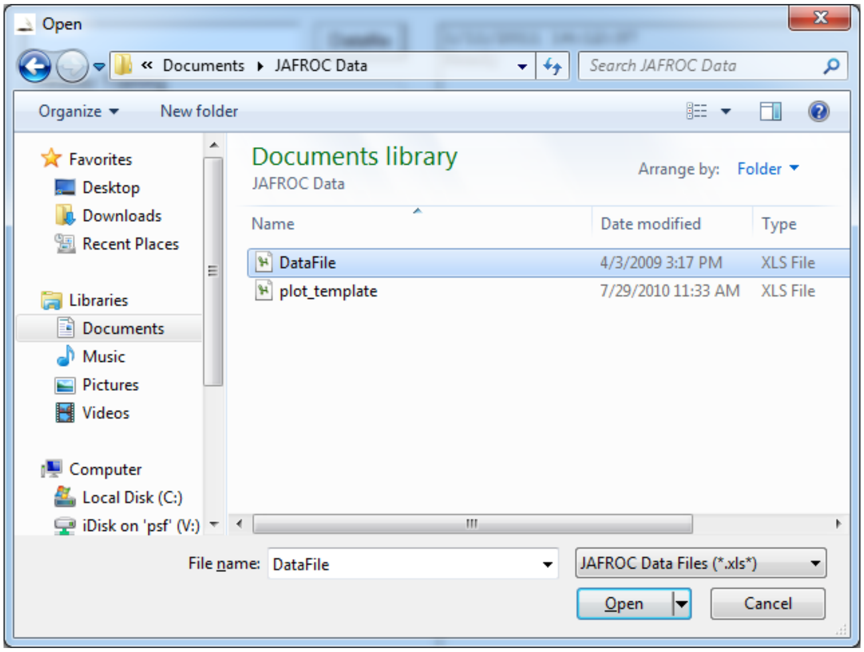


The following screen will show. Click on the “Datafile” button located at top-left.



```
1/11/2011 14:12:37
Ready
```

Locate your data file in “Documents\JAFROC Data” folder. Select your data file and double click or click “Open”.

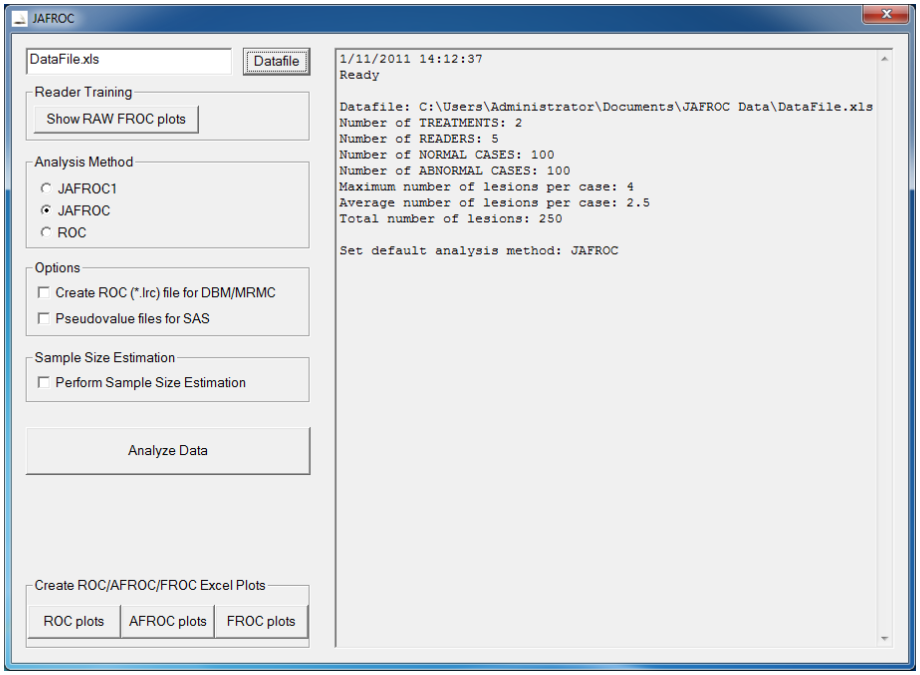


Name	Date modified	Type
DataFile	4/3/2009 3:17 PM	XLS File
plot_template	7/29/2010 11:33 AM	XLS File

File name: DataFile

JAFROC Data Files (*.xls*)

If there are errors (e.g., the selected file is not a valid input file or the data is inconsistent) the program will display appropriate error messages on the console. Otherwise the screen will show the following.



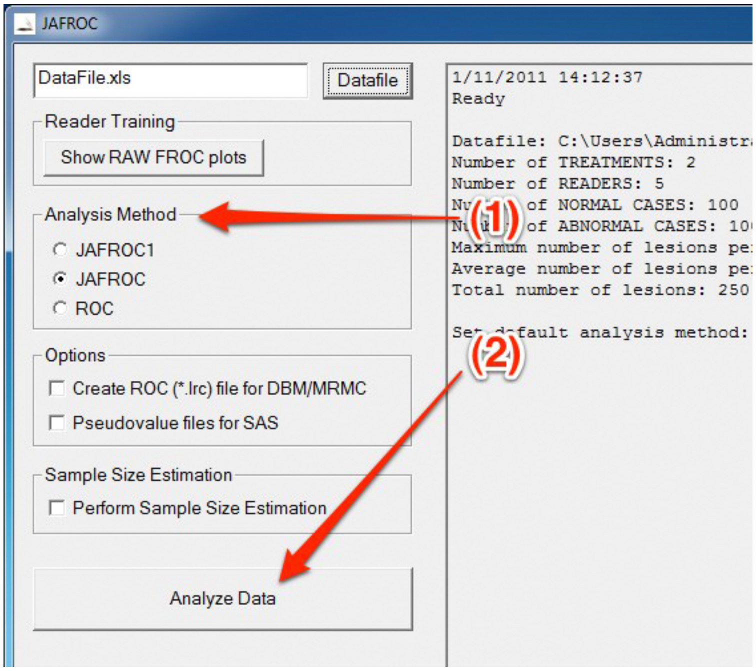
DataFile.xls

○ JAFROC1
● JAFROC
○ ROC

☐ Create ROC (*.lrc) file for DBM/MRMC
☐ Pseudovalue files for SAS

☐ Perform Sample Size Estimation

```
1/11/2011 14:12:37
Ready

Datafile: C:\Users\Administrator\Documents\JAFROC Data\DataFile.xls
Number of TREATMENTS: 2
Number of READERS: 5
Number of NORMAL CASES: 100
Number of ABNORMAL CASES: 100
Maximum number of lesions per case: 4
Average number of lesions per case: 2.5
Total number of lesions: 250

Set default analysis method: JAFROC
```



DataFile.xls

○ JAFROC1
● JAFROC
○ ROC

☐ Create ROC (*.lrc) file for DBM/MRMC
☐ Pseudovalue files for SAS

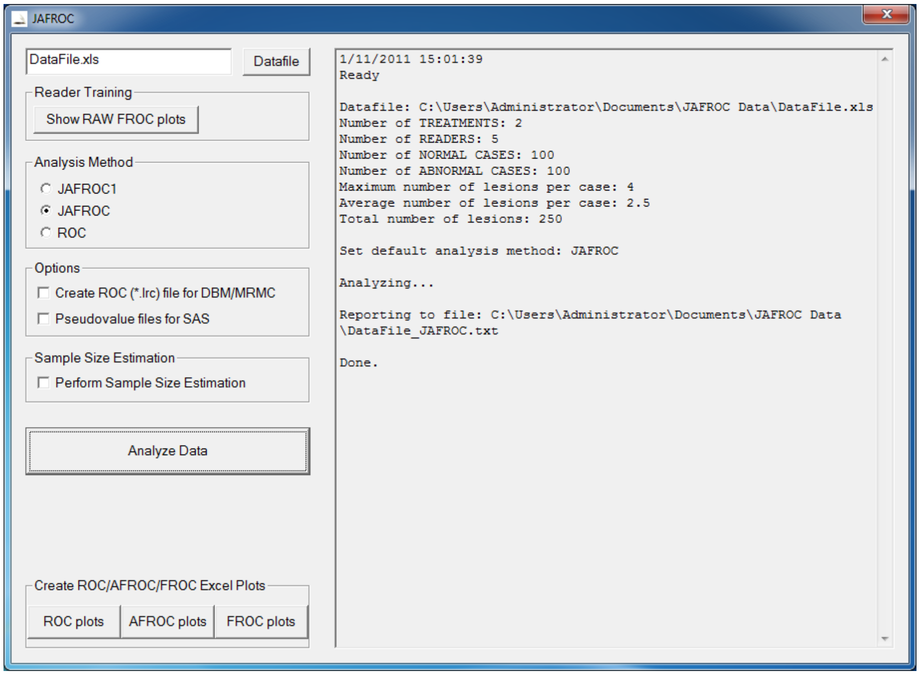
☐ Perform Sample Size Estimation

```
1/11/2011 14:12:37
Ready

Datafile: C:\Users\Administr
Number of TREATMENTS: 2
Number of READERS: 5
Nu      of NORMAL CASES: 100
Nu      of ABNORMAL CASES: 10
Maximum number of lesions pe
Average number of lesions pe
Total number of lesions: 250

Se   -fault analysis method:
```

(1) First, select the analysis option. The simplest way is to keep the defaults.

(2) Then click on "Analyze Data" button.

Upon successful completion the following will show



DataFile.xls

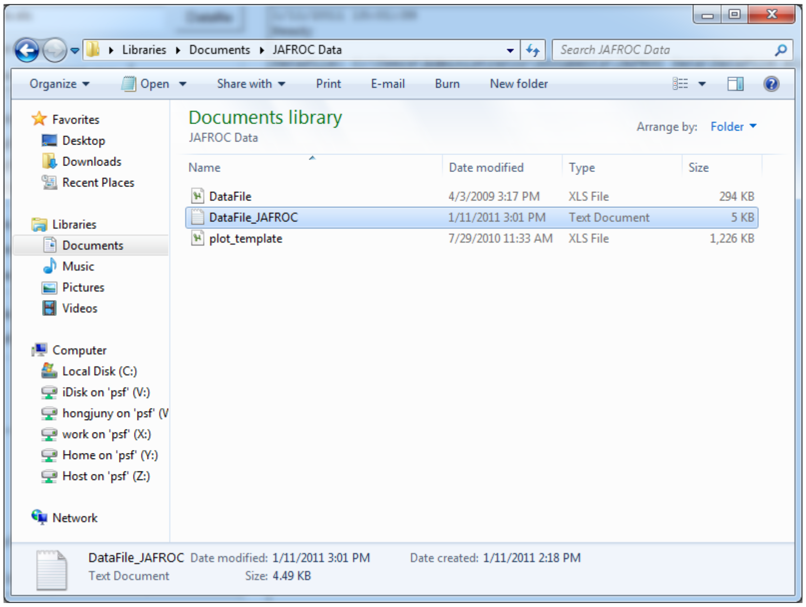
○ JAFROC1
● JAFROC
○ ROC

☐ Create ROC (*.lrc) file for DBM/MRMC
☐ Pseudovalue files for SAS

☐ Perform Sample Size Estimation

```
1/11/2011 15:01:39
Ready

Datafile: C:\Users\Administrator\Documents\JAFROC Data\DataFile.xls
Number of TREATMENTS: 2
Number of READERS: 5
Number of NORMAL CASES: 100
Number of ABNORMAL CASES: 100
Maximum number of lesions per case: 4
Average number of lesions per case: 2.5
Total number of lesions: 250

Set default analysis method: JAFROC

Analyzing...

Reporting to file: C:\Users\Administrator\Documents\JAFROC Data
\DataFile_JAFROC.txt

Done.
```

Open the JAFROC Data folder.



Name	Date modified	Type	Size
DataFile	4/3/2009 3:17 PM	XLS File	294 KB
DataFile_JAFROC	1/11/2011 3:01 PM	Text Document	5 KB
plot_template	7/29/2010 11:33 AM	XLS File	1,226 KB

DataFile_JAFROC Date modified: 1/11/2011 3:01 PM Date created: 1/11/2011 2:18 PM
Text Document Size: 4.49 KB

The output file is DataFile_JAFROC.txt. It will contain the following (for the sample data set):

Output file for the sample data set

```
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IMPLIED, INCLUDING BUT NOT LIMITED TO THE WARRANTIES OF MERCHANTABILITY,

FITNESS FOR A PARTICULAR PURPOSE AND NONINFRINGEMENT. IN NO EVENT SHALL THE

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LIABILITY, WHETHER IN AN ACTION OF CONTRACT, TORT OR OTHERWISE, ARISING FROM,

OUT OF OR IN CONNECTION WITH THE SOFTWARE OR THE USE OR OTHER DEALINGS

IN THE SOFTWARE.


================================================================================


 JAFROC Version 4.0

 Last Compilation Date

 JAFROC_CORE.DLL : Jan 10 2011 12:34:00

 JAFROC.EXE      : Jan 11 2011 12:27:18


================================================================================


 This run date: 1/11/2011 15:01:46




 Input  Data Filename :     DataFile.xls

 Output Data Filename :     DataFile_JAFROC.txt




 Analysis method:         :  JAFROC FOM DBM-MRMC SIGNIFICANCE TESTING

 Number of Readers        :  5

 Number of Treatments     :  2

 Number of Normal Cases   :  100
```

```
 Number of Abnormal Cases :  100

 fraction normal cases    :  0.500

 min    LESIONS_PER_IMAGE :  1

 max    LESIONS_PER_IMAGE :  4

 mean   LESIONS_PER_IMAGE :  2.5

 Total  LESIONS           :  250

 Inc. Loc. Frac.          :  0.031


================================================================================


For TRT = 1         , and RDR = 1         , max FPF =  0.990.

For TRT = 1         , and RDR = 2         , max FPF =  0.990.

For TRT = 1         , and RDR = 3         , max FPF =  1.000.

For TRT = 1         , and RDR = 4         , max FPF =  0.990.

For TRT = 1         , and RDR = 5         , max FPF =  0.990.

For TRT = 2         , and RDR = 1         , max FPF =  1.000.

For TRT = 2         , and RDR = 2         , max FPF =  1.000.

For TRT = 2         , and RDR = 3         , max FPF =  1.000.

For TRT = 2         , and RDR = 4         , max FPF =  1.000.

For TRT = 2         , and RDR = 5         , max FPF =  1.000.


================================================================================


 FOM = Trapezoidal area under AFROC curve, ignoring NLs on abnormal cases



 FOMs for TREATMENTS (columns) and READERS (rows)



              1          2

              ------     ------
```

```
1             0.6654     0.6486

2             0.6867     0.6963

3             0.7447     0.7067

4             0.7118     0.7602

5             0.6416     0.7416


==================  Results: RANDOM_ALL  ==================




 F-statistic and p-value



 Significance level of test (alpha) = 0.05

 F-statistic  :      0.382

 p-value      : 5.469E-001

 DF (Num,Den) : (  1, 1.370E+001 )



 N.B. If the p-value is less than 0.05 there is a significant difference

      between at least one pair of TREATMENTS



 READER-averaged FOMs for TREATMENTS and 95% confidence intervals:



1           0.6901, ( 0.6286, 0.7515)

2           0.7107, ( 0.6506, 0.7708)



 INTER-TREATMENT differences and 95% confidence intervals:



 FOM(1) - FOM(2) = -0.0206, (-0.0923, 0.0511 )





 Variance components needed for sample-size estimation:

   var_tr  :  1.2143E-003
```

```
   var_tc  :  5.1149E-002

   var_trc :  5.7859E-002



==================  Results: RANDOM_CASES  ==================



 F-statistic and p-value


 Significance level of test (alpha) = 0.05

 F-statistic  :      0.677

 p-value      : 4.116E-001

 DF (Num,Den) : (  1, 1.990E+002 )


 N.B. If the p-value is less than 0.05 there is a significant difference

      between at least one pair of TREATMENTS


 READER-averaged FOMs for TREATMENTS and 95% confidence intervals:


1           0.6901, ( 0.6390, 0.7411)

2           0.7107, ( 0.6649, 0.7565)


 INTER-TREATMENT differences and 95% confidence intervals:


 FOM(1) - FOM(2) = -0.0206, (-0.0700, 0.0288 )




==================  Results: RANDOM_RDRS  ==================
```

```
 F-statistic and p-value


 Significance level of test (alpha) = 0.05
 F-statistic  :      0.706
 p-value      : 4.480E-001
 DF (Num,Den) : (  1, 4.000E+000 )


 N.B. If the p-value is less than 0.05 there is a significant difference
      between at least one pair of TREATMENTS


 READER-averaged FOMs for TREATMENTS and 95% confidence intervals:


1           0.6901, ( 0.6403, 0.7398)
2           0.7107, ( 0.6570, 0.7644)


 INTER-TREATMENT differences and 95% confidence intervals:


 FOM(1) - FOM(2) = -0.0206, (-0.0887, 0.0475 )



================================================================================
```

Interpretation of the output file

```
Inc. Loc. Frac.          :  0.031
```

This is the incorrect localization fraction (ILF): the fraction of abnormal images on which the highest rated location was a false positive (and not a lesion). See my 2004 Med Phys paper. If ILF is large then one expects a large power advantage of JAFROC over ROC analysis. If it is zero, one does not expect a power advantage and you might as well analyze your data with DBM_MRMC software.

```
==================  Results: RANDOM_ALL  ==================



 F-statistic and p-value


 Significance level of test (alpha) = 0.05

 F-statistic  :      0.382

 p-value      : 5.469E-001

 DF (Num,Den) : (  1, 1.370E+001 )


 N.B. If the p-value is less than 0.05 there is a significant difference

      between at least one pair of TREATMENTS
```

If p < 0.05 you have a significant difference.

```
READER-averaged FOMs for TREATMENTS and 95% confidence intervals:


1           0.6901, ( 0.6286, 0.7515)
```

```
2           0.7107, ( 0.6506, 0.7708)
```

Lists the reader-averaged figures of merit for the 2 treatments (modalities) and 95% confidence intervals. The confidence intervals have not been corrected for multiple comparisons.

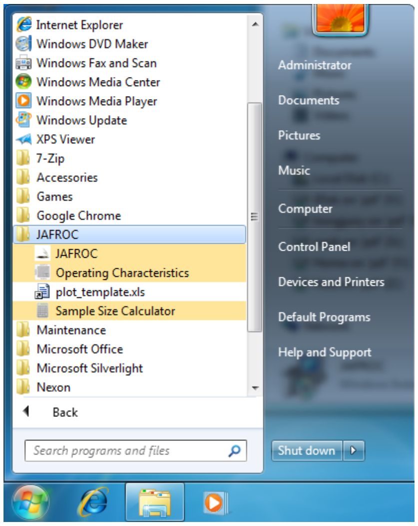
```
INTER-TREATMENT differences and 95% confidence intervals:

 FOM(1) - FOM(2) = -0.0206, (-0.0923, 0.0511 )
```

Lists the inter-treatment differences between reader-averaged figures of merit for all pairings of the treatments and 95% confidence intervals for the differences. If the 95% CI does not include 0, then the corresponding modality pairs are significantly different. The confidence intervals have not been corrected for multiple comparisons (more than one pair). If they had been, the corrected CI's would be larger and you would see fewer significant differences. But if p < 0.05 at least one of the differences is significant.

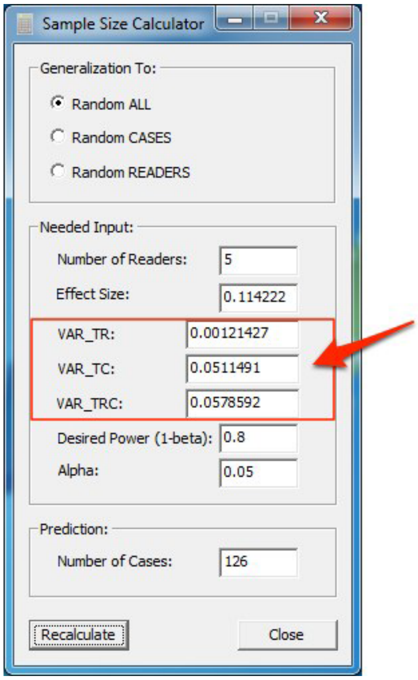
```
Variance components needed for sample-size estimation:

   var_tr  :  1.2143E-003

   var_tc  :  5.1149E-002

   var_trc :  5.7859E-002
```

ROC sample size calculator

[This could be used for sample size estimation for JAFROC but you don't know the JAFROC effect size corresponding to a given ROC effect size, so it is best to use the built in capability in JAFROC described after this section.] This is an implementation of the Hillis Berbaum method (8). Click [Start] menu and select the “Sample Size Calculator” icon.



The following screen will show. Enter the three variance components, set the appropriate parameters, and press [Recalculate].


Sample Size Calculator

Generalization To:

● Random ALL
○ Random CASES
○ Random READERS

Needed Input:

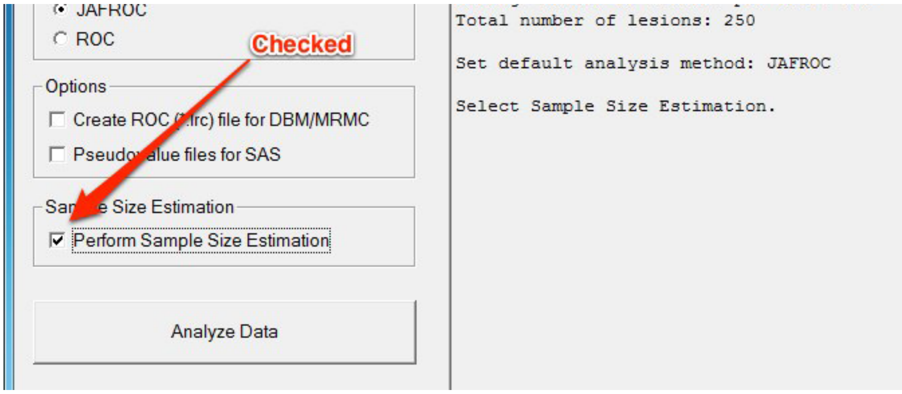
Number of Readers: 5
Effect Size: 0.114222
VAR_TR: 0.00121427
VAR_TC: 0.0511491
VAR_TRC: 0.0578592
Desired Power (1-beta): 0.8
Alpha: 0.05

Prediction:

Number of Cases: 126

JAFROC sample size calculator

If you had selected "Perform Sample Size Estimation" in the main screen, repeated below, the program will walk you through one more step. You will not have to re-enter the variance components manually.



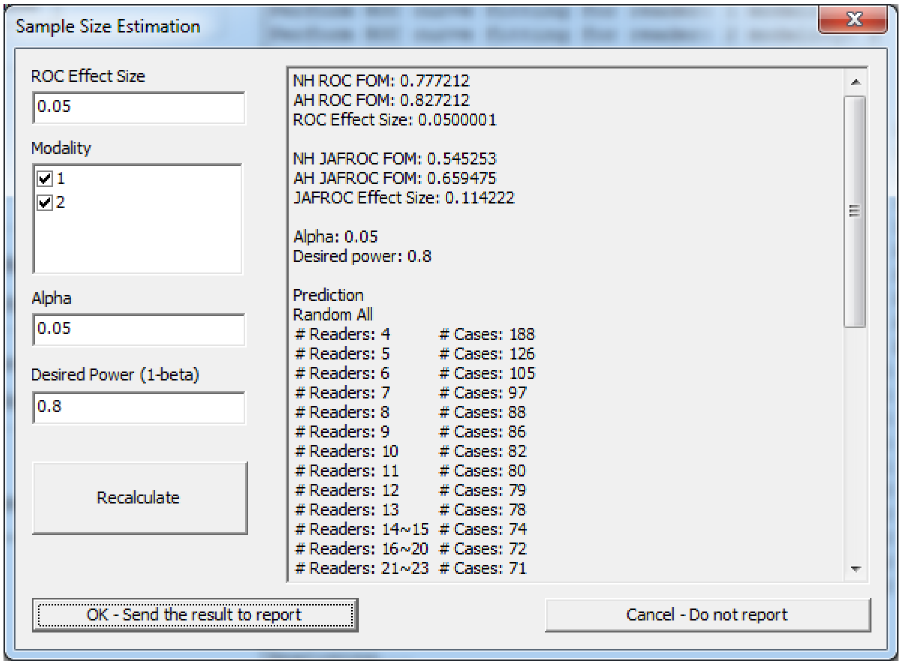
● JAFROC
○ ROC

☐ Create ROC (.lrc) file for DBM/MRMC
☐ Pseudovalue files for SAS

☑ Perform Sample Size Estimation

```
Total number of lesions: 250

Set default analysis method: JAFROC

Select Sample Size Estimation.
```

Upon the “Sample Size Estimation” screen, you will enter appropriate parameters as for your request, then click on “Recalculate” button. Required number of cases per number of readers will be shown. Press “OK” to report the result.



ROC Effect Size: 0.05

Modality: ☑ 1 ☑ 2

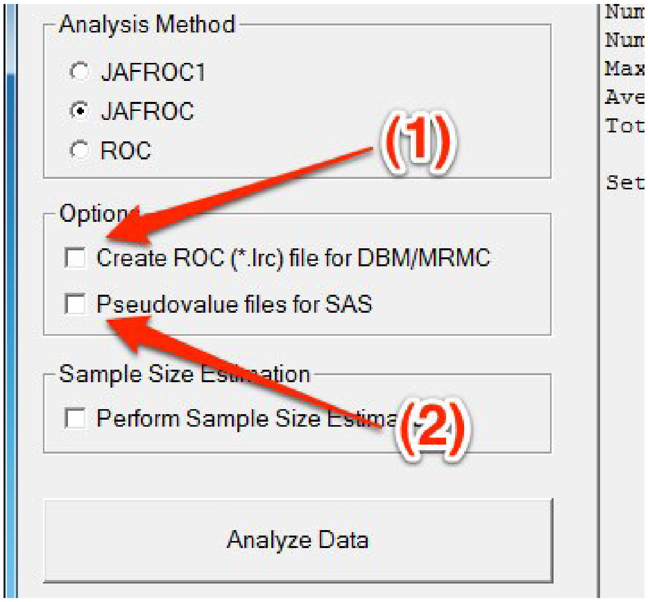
Alpha: 0.05

Desired Power (1-beta): 0.8

```
NH ROC FOM: 0.777212
AH ROC FOM: 0.827212
ROC Effect Size: 0.0500001

NH JAFROC FOM: 0.545253
AH JAFROC FOM: 0.659475
JAFROC Effect Size: 0.114222

Alpha: 0.05
Desired power: 0.8

Prediction
Random All
# Readers: 4       # Cases: 188
# Readers: 5       # Cases: 126
# Readers: 6       # Cases: 105
# Readers: 7       # Cases: 97
# Readers: 8       # Cases: 88
# Readers: 9       # Cases: 86
# Readers: 10      # Cases: 82
# Readers: 11      # Cases: 80
# Readers: 12      # Cases: 79
# Readers: 13      # Cases: 78
# Readers: 14~15  # Cases: 74
# Readers: 16~20  # Cases: 72
# Readers: 21~23  # Cases: 71
```

The rest of the output is for random cases and random readers analyses, as per the DBM-MRMC documentation (9).

Options

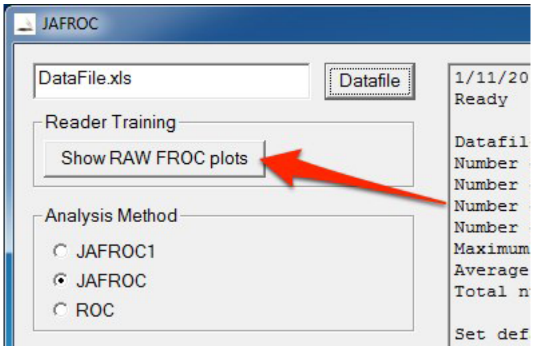


(1) Convert FROC data into ROC and save it to the file compatible to DBM-MRMC software (*.lrc).

(2) Save pseudo-values to a file in plain text format, consists of four columns of numbers. For each row, there are Reader Index, Treatment Index, Case Index, and the corresponding pseudo-value.

Plots

Press “Show RAW FROC plots” button in the Reader Training section.

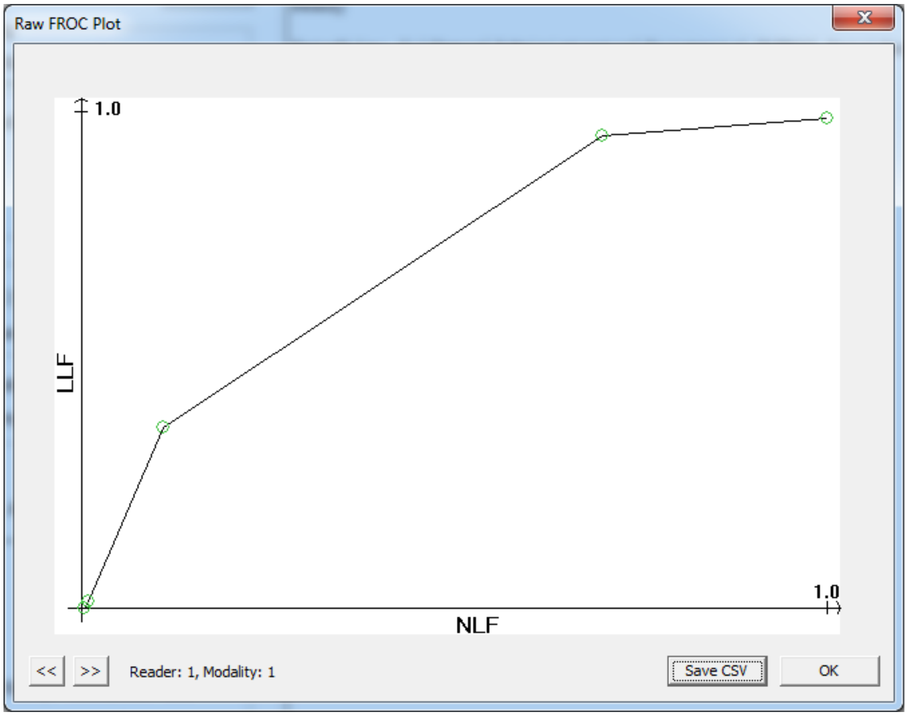


DataFile.xls

○ JAFROC1
● JAFROC
○ ROC

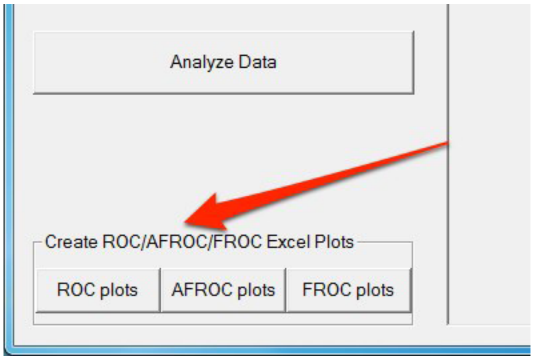
```
1/11/20
Ready

Datafil
Number
Number
Number
Number
Maximum
Average
Total n

Set def
```

Shown is the raw FROC plot for each reader and modality. Press << and >> button to browse other reader and modality. Or, you can save the raw plot as CSV file.

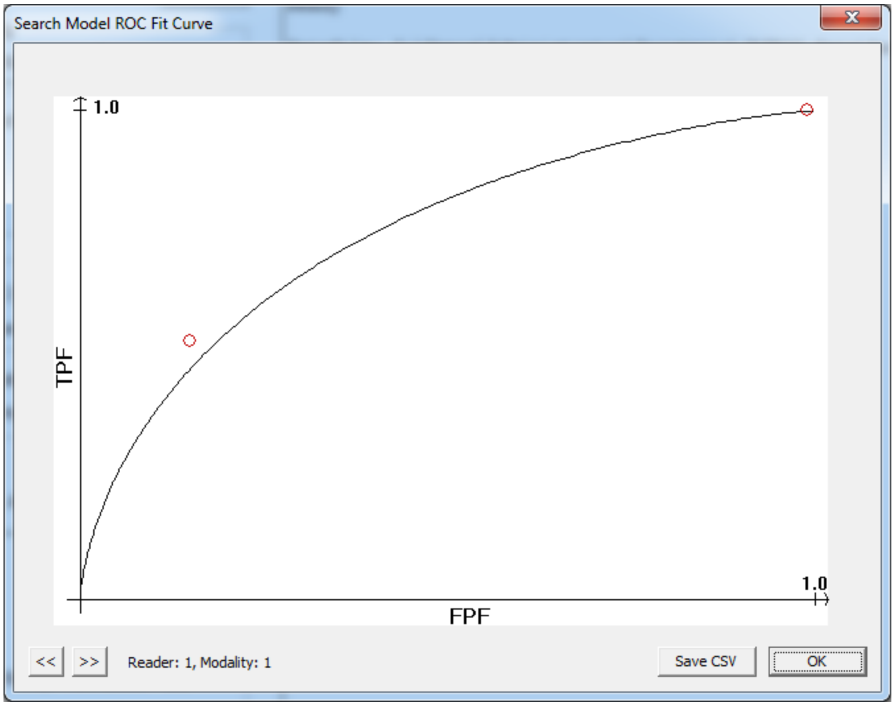


Reader: 1, Modality: 1

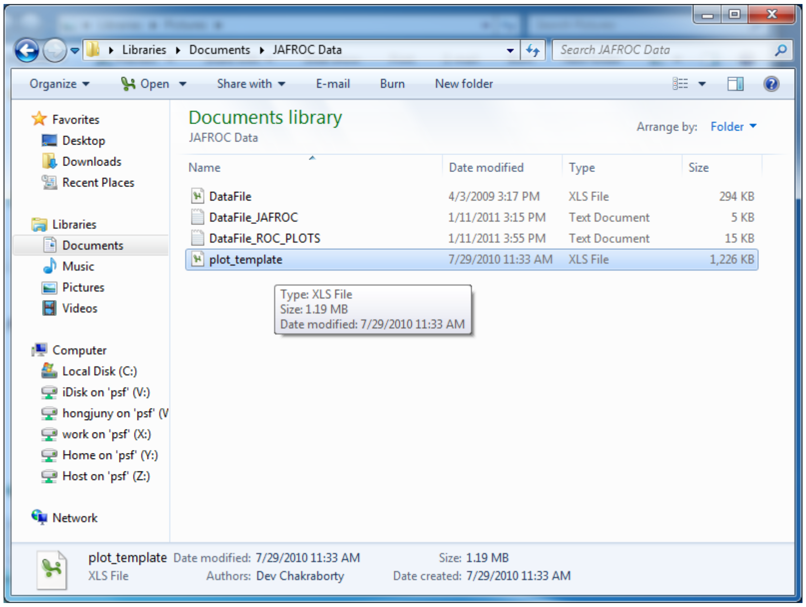
Press “ROC plots”, “AFROC plots”, and/or “FROC plots” button in the “Create ROC/AFROC/FROC Excel Plots” section.



Shown is the Search Model fitted curve for each reader and modality. Press << and >> button to browse other reader and modality. Or, you can save the raw plot as CSV file.



Also, the search model fitted curves for every reader and modality pairs can be shown in Excel worksheet. Open the JAFROC Data folder.

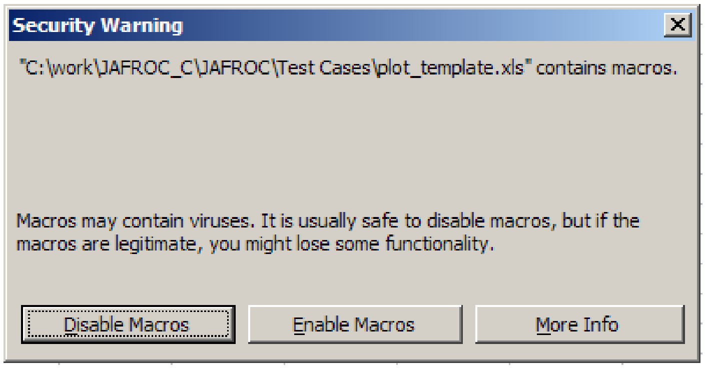


Name	Date modified	Type	Size
DataFile	4/3/2009 3:17 PM	XLS File	294 KB
DataFile_JAFROC	1/11/2011 3:15 PM	Text Document	5 KB
DataFile_ROC_PLOTS	1/11/2011 3:55 PM	Text Document	15 KB
plot_template	7/29/2010 11:33 AM	XLS File	1,226 KB

Type: XLS File
Size: 1.19 MB
Date modified: 7/29/2010 11:33 AM

plot_template Date modified: 7/29/2010 11:33 AM Size: 1.19 MB
XLS File Authors: Dev Chakraborty Date created: 7/29/2010 11:33 AM

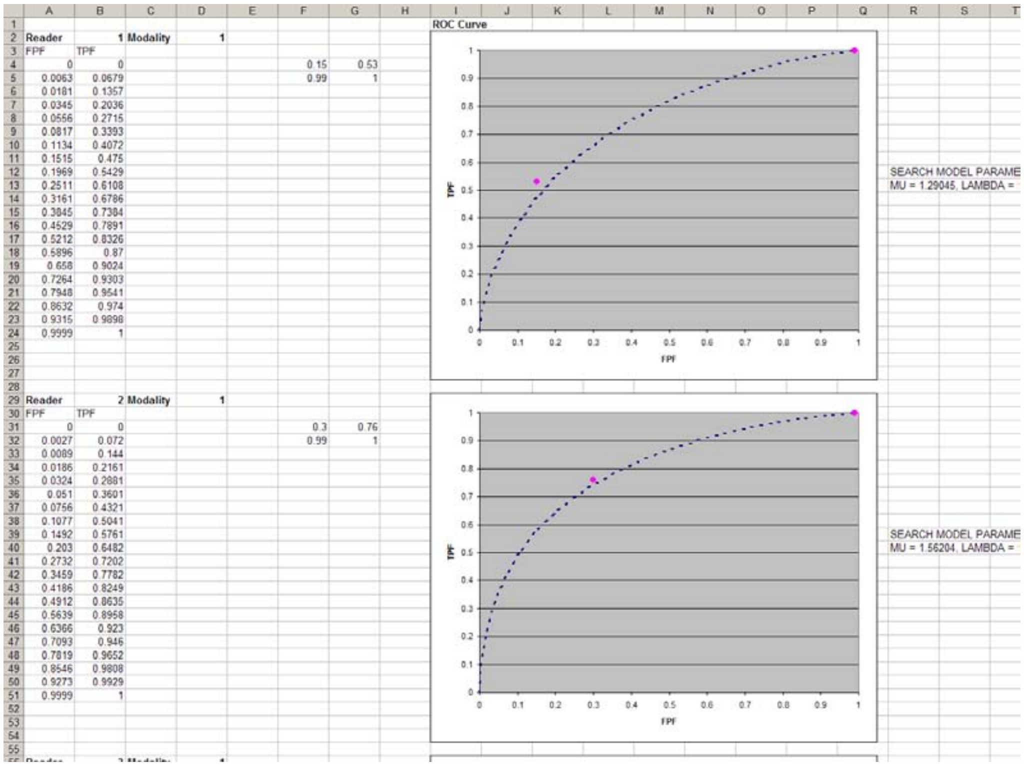
The file “plot_template.xls” file includes script to read the search model fitted plots data file “DataFile_ROC_PLOTS.txt”. Double-click on “plot_template.xls”, and press “Enable Macros” to allow the script to run reading plots.



"C:\work\JAFROC_C\JAFROC\Test Cases\plot_template.xls" contains macros.

Macros may contain viruses. It is usually safe to disable macros, but if the macros are legitimate, you might lose some functionality.

Select “DataFile_ROC_PLOTS.txt”. Search model fitted ROC curves will be shown on the worksheet, along with the fitted search model parameters.



	A	B	C	D	E	F	G
1							
2	**Reader**	**1**	**Modality**	**1**			
3	FPF	TPF					
4	0	0				0.15	0.53
5	0.0063	0.0679				0.99	1
6	0.0181	0.1357					
7	0.0345	0.2036					
8	0.0556	0.2715					
9	0.0817	0.3393					
10	0.1134	0.4072					
11	0.1515	0.475					
12	0.1969	0.5429					
13	0.2511	0.6108					
14	0.3161	0.6786					
15	0.3845	0.7384					
16	0.4529	0.7891					
17	0.5212	0.8326					
18	0.5896	0.87					
19	0.658	0.9024					
20	0.7264	0.9303					
21	0.7948	0.9541					
22	0.8632	0.974					
23	0.9315	0.9898					
24	0.9999	1					
25							
26							
27							
28							
29	**Reader**	**2**	**Modality**	**1**			
30	FPF	TPF					
31	0	0				0.3	0.76
32	0.0027	0.072				0.99	1
33	0.0089	0.144					
34	0.0186	0.2161					
35	0.0324	0.2881					
36	0.051	0.3601					
37	0.0756	0.4321					
38	0.1077	0.5041					
39	0.1492	0.5761					
40	0.203	0.6482					
41	0.2732	0.7202					
42	0.3459	0.7782					
43	0.4186	0.8249					
44	0.4912	0.8635					
45	0.5639	0.8958					
46	0.6366	0.923					
47	0.7093	0.946					
48	0.7819	0.9652					
49	0.8546	0.9808					
50	0.9273	0.9929					
51	0.9999	1					
52							
53							
54							
55							

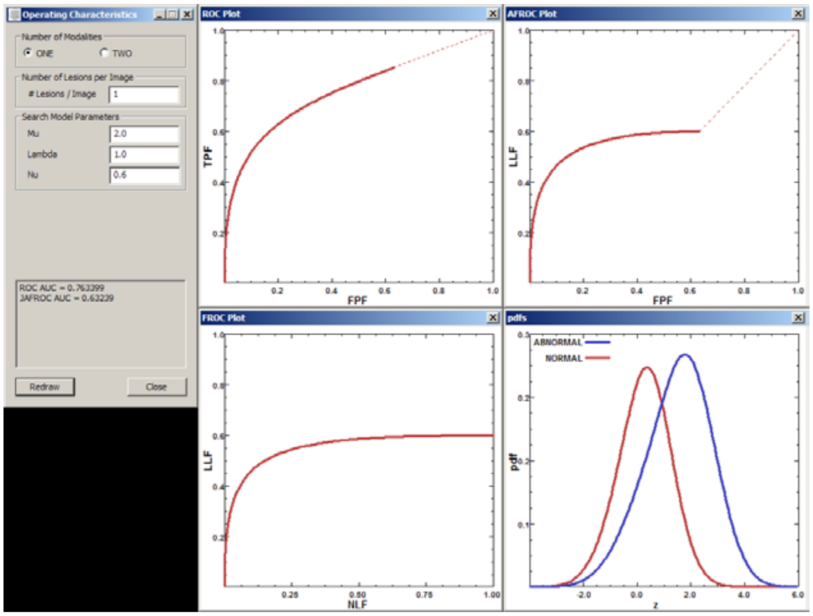
SEARCH MODEL PARAME
MU = 1.29045, LAMBDA =

SEARCH MODEL PARAME
MU = 1.56204, LAMBDA =

Operating Characteristics

This is a convenient way to visualize ROC, AFROC, and FROC plots for specific search model parameters, to observe the differences between treatments, and calculate ROC and JAFROC figures of merit.

One modality



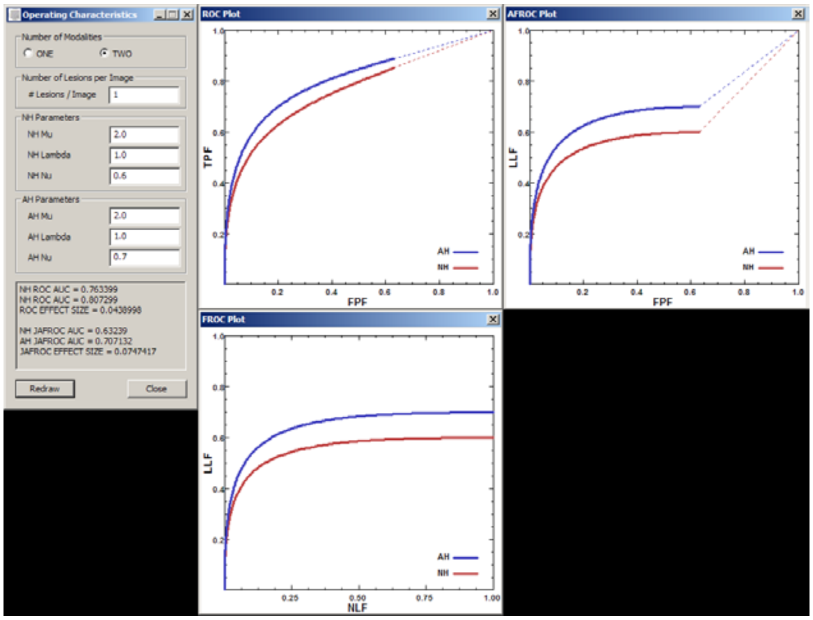
Number of Modalities
● ONE ○ TWO

Number of Lesions per Image
Lesions / Image: 1

Search Model Parameters
Mu: 2.0
Lambda: 1.0
Nu: 0.6

```
ROC AUC = 0.763399
JAFROC AUC = 0.63239
```

Two modalities



Number of Modalities
○ ONE ● TWO

Number of Lesions per Image
Lesions / Image: 1

NH Parameters
NH Mu: 2.0
NH Lambda: 1.0
NH Nu: 0.6

AH Parameters
AH Mu: 2.0
AH Lambda: 1.0
AH Nu: 0.7

```
NH ROC AUC = 0.763399
NH ROC AUC = 0.807299
ROC EFFECT SIZE = 0.0438998

NH JAFROC AUC = 0.63239
AH JAFROC AUC = 0.707132
JAFROC EFFECT SIZE = 0.0747417
```

If warnings or errors during the analysis, error message is displayed on console window. If you cannot fix the problem send me the data file. Please bring errors on screen to my attention.

Good luck!

Dev P. Chakraborty

Last revision: 1/18/2011

References

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5. Bunch PC, Hamilton JF, Sanderson GK, Simmons AH. A Free-Response Approach to the Measurement and Characterization of Radiographic-Observer Performance. J of Appl Photogr Eng. 1978; 4(4):166-71.
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